Appendix A

OM protein - protein search, using sw model

Copyright (c) 1993 - 2000 Compugen Ltd.

GenCore version 4.5

Run on: February 21, 2002, 08:48:04 ; Search time 39.64 Seconds
                                              (without alignments)
                                              10.218 Million cell updates/sec

Title:
Perfect score: 94
Sequence: 1 GLEISEEINEEDLKECFF 18

Scoring table: BLOSUM62
                     Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
                 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                SUMMARIES

                                    %
Result   Query
No.   Score   Match   Length   DB   ID   Description
------ -----   -----   ------   --   --   -----------
1   94   100.0   1480   1   US-08-466-886-17   Sequence 17, Appl
                                                           Sequence 2, Appl

        Qy   1 GLEISEEINEEDLKECFF 18
                    |||||||||||||||||||
        Db   817 GLEISEEINEEDLKECFF 834

ALIGNMENTS

RESULT 1
US-08-466-886-17
Sequence 17, Application US/08466886
; Patent No. 5776677
; GENERAL INFORMATION:
;   APPLICANT: Tsui, Lap-Chee
;   APPLICANT: Riordan, John R.
;   APPLICANT: Rommens, Johanna M.
;   APPLICANT: Kerem, Bat-Sheva
;   APPLICANT: Collins, Francis S.
;   APPLICANT: Iannuzzi, Michael C.
;   APPLICANT: Drumm, Mitchell L.
;   APPLICANT: Buckwald, Manuel
;   TITLE OF INVENTION: Cystic Fibrosis Gene
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
;   STREET: 1100 New York Avenue, N.W.
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA
;   ZIP: 20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/466,886
;   FILING DATE: 06-JUN-1995
;   CLASSIFICATION: 435
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Goldstein, Jorge A.
;   REGISTRATION NUMBER: 29,021
;   REFERENCE/DOCKET NUMBER: 1329.0010006
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 202-371-2600
;   TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 17:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1480 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-466-886-17

Query Match   100.0%; Score 94; DB 1; Length 1480;
Best Local Similarity   100.0%; Pred. No. 2.3e-05;
Matches   18; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: February 21, 2002, 08:53:13 ; Search time 39.64 Seconds
                                              (without alignments)
                                              12.489 Million cell updates/sec

Title: US-09-512-260-2
Perfect score: 116
Sequence: 1 GLEISEEINEEDLKECFFDDME 22

Scoring table: BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
                2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
                3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
                4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
                5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
                6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred.   No. is the number of results predicted by chance to have a
score   greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

                        %
Result   Query   Match   Length DB   ID   Description
No.   Score

  1   116   100.0   1480   1   US-08-466-886-17   Sequence 17, Appl

Qy   1 GLEISEEINEEDLKECFFDDME 22
          |||||||||||||||||||||
Db   817 GLEISEEINEEDLKECFFDDME 838

ALIGNMENTS

RESULT   1
US-08-466-886-17
Sequence 17, Application US/08466886
Patent No. 5776677
GENERAL INFORMATION:
  APPLICANT: Tsui, Lap-Chee
  APPLICANT: Riordan, John R.
  APPLICANT: Rommens, Johanna M.
  APPLICANT: Kerem, Bat-Sheva
  APPLICANT: Collins, Francis S.
  APPLICANT: Iannuzzi, Michael C.
  APPLICANT: Drumm, Mitchell L.
  APPLICANT: Buckwald, Manuel
  TITLE OF INVENTION: Cystic Fibrosis Gene
  NUMBER OF SEQUENCES: 43
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
    STREET: 1100 New York Avenue, N.W.
    CITY: Washington
    STATE: DC
    COUNTRY: USA
    ZIP: 20005
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    OPERATING SYSTEM: PC-DOS/MS-DOS
    SOFTWARE: PatentIn Release #1.0, Version #1.30
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/466,886
    FILING DATE: 06-JUN-1995
    CLASSIFICATION: 435
  ATTORNEY/AGENT INFORMATION:
    NAME: Goldstein, Jorge A.
    REGISTRATION NUMBER: 29,021
    REFERENCE/DOCKET NUMBER: 1329.0010006
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: 202-371-2600
    TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 17:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1480 amino acids
    TYPE: amino acid
    TOPOLOGY: linear
  MOLECULE TYPE: protein
US-08-466-886-17

Query Match   100.0%; Score 116; DB 1; Length 1480;
Best Local Similarity 100.0%; Pred. No. 6.4e-08;
Matches   22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Appendix C

```
                    GenCore version 4.5
            Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on:        February 21, 2002, 08:53:17 ; Search time 39.64 Seconds
                                             (without alignments)
                                             15.328 Million cell updates/sec

Title:         US-09-512-260-4
Perfect score: 133
Sequence:      1 GWTLNSAGYLLGKINLKALPAALAKKIL 27

Scoring table: BLOSUM62

Searched:      Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:  212252

Searched:      212252 seqs, 22503292 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :     Issued_Patents_AA:*
               1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
               2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
               3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
               4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
               5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
               6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                         SUMMARIES
Result            Query                                        %
 No.   Score   Match Length   DB   ID                    Description
-----  -----   ------------  ----  -------------------   ---------------
  1    133     100.0    27    3    US-09-116-294-3       Sequence 3, Appli
```

ALIGNMENTS

```
RESULT   1
US-09-116-294-3
; Sequence 3, Application US/09116294
; Patent No. 6025140
; GENERAL INFORMATION:
; APPLICANT: Langel, Ulo
; APPLICANT: Bartfai, Tamas
; APPLICANT: Pooga, Margus
; APPLICANT: Valkna, Andres
; APPLICANT: Saar, Kulliki
; APPLICANT: Hallbrink, Mattias
; TITLE OF INVENTION: Conjugated Constructs of Peptides and
; TITLE OF INVENTION: Nucleic Acid Analogs, and Their Transport Across Membranes
; FILE REFERENCE: 4394
; CURRENT APPLICATION NUMBER: US/09/116,294
; CURRENT FILING DATE: 1998-07-16
; EARLIER APPLICATION NUMBER: 60/052,678
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: PRT
; ORGANISM: k:\asp
US-09-116-294-3

Query Match             100.0%;  Score 133;  DB 3;  Length 27;
Best Local Similarity   100.0%;  Pred. No. 8.8e-15;
Matches    27;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 GWTLNSAGYLLGKINLKALPAALAKKIL 27
              |||||||||||||||||||||||||||||
Db          1 GWTLNSAGYLLGKINLKALPAALAKKIL 27
```

Appendix D

OM protein - protein search, using sw model

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

Run on: February 21, 2002, 08:53:17 ; Search time 39.64 Seconds
(without alignments)
9.083 Million cell updates/sec

Title:	US-09-512-260-5
Perfect score:	92
Sequence:	1 RQIKIWFQNRRMKWKK 16

Scoring table:	BLOSUM62
	Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	%	Query Match	Length	DB	ID	Description
6	92	100.0	16	3		US-09-116-294-4	Sequence 4, Appli...

RESULT 1
US-08-928-958-7
Sequence 7, Application US/08928958
Patent No. 5877282

GENERAL INFORMATION:
APPLICANT: NADLER, STEVEN G.
APPLICANT: CLEAVELAND, JEFFREY S.
APPLICANT: BLAKE, JAMES
APPLICANT: HAFFAR, OMAR K.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF NUCLEAR PROTEIN
TITLE OF INVENTION: TRANSLOCATION HAVING NUCLEAR LOCALIZATION SEQUENCES AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBINS & ASSOCIATES
STREET: 90 MIDDLEFIELD ROAD, SUITE 200
CITY: MENLO PARK
STATE: CA
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,958
FILING DATE: 12-SEP-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026978
FILING DATE: 20-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5998-0019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 325-7812
TELEFAX: (650) 325-7823
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

ALIGNMENTS

US-08-928-958-7

Query Match   100.0%; Score 92; DB 2; Length 16;